

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 04:22:25 ; Search time 2763 Seconds
(without alignments)
15046.897 Million cell

updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc.....aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description

1	828	96.5	1624	9	HUMERPR	M34986 Human
eryth						
2	828	96.5	1818	6	AX658275	AX658275
Sequence						
3	828	96.5	1818	9	HUMERYTH	M60459 Human
eryth						
4	826.4	96.3	1527	6	AR062465	AR062465
Sequence						
5	824.8	96.1	1317	6	AR202361	AR202361
Sequence						
6	824.8	96.1	1317	6	AX008198	AX008198
Sequence						
7	820	95.6	1317	6	AR202362	AR202362
Sequence						
8	820	95.6	1317	6	AX008201	AX008201
Sequence						
9	818.4	95.4	1848	6	CQ724319	CQ724319
Sequence						
10	750.4	87.5	4990	6	AR119365	AR119365
Sequence						
11	750	87.4	750	6	AR031378	AR031378
Sequence						
12	750	87.4	750	6	BD134377	BD134377
Peptide 1						
13	750	87.4	750	6	AR428937	AR428937
Sequence						
14	750	87.4	750	6	BD009746	BD009746
Compositi						
15	748.2	87.2	6256	6	BD168201	BD168201
Method of						
16	741	86.4	5565	6	BD168199	BD168199
Method of						
17	702	81.8	1666	6	BD090961	BD090961
Assay emp						
18	610	71.1	1843	4	AF274305	AF274305 Sus
scrof						
19	577.6	67.3	2154	9	BC019092	BC019092
Homo sapi						
20	577.6	67.3	5761	9	AK074082	AK074082
Homo sapi						
21	576.4	67.2	5683	6	AX554424	AX554424
Sequence						
22	576.4	67.2	6122	6	AX554413	AX554413
Sequence						
23	576.4	67.2	6122	6	AX554422	AX554422
Sequence						
24	576.4	67.2	6122	6	AX642149	AX642149
Sequence						
25	576.4	67.2	6125	6	AX554420	AX554420
Sequence						
26	576.2	67.2	1741	10	MUSERPR	J04843
Mouse eryth						
27	576	67.1	4883	6	AX600116	AX600116
Sequence						
28	574.6	67.0	1769	10	BC046282	BC046282
Mus muscu						

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 04:18:19 ; Search time 406 Seconds
(without alignments)
12510.192 Million cell

updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgctc.....aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	828	96.5	1024	10	ABZ83469	Abz83469
Toxicolog						
2	828	96.5	1527	2	AAQ82990	Aaq82990
Human ery						
3	828	96.5	1733	10	ADE28670	Ade28670
Human NOV						
4	828	96.5	1733	10	ADE28672	Ade28672
Human NOV						
5	828	96.5	1733	12	ADM93417	Adm93417
Human NOV						
6	828	96.5	1733	12	ADM93415	Adm93415
Human NOV						
7	828	96.5	1848	13	ADQ83546	Adq83546
Human tum						
8	828	96.5	1849	12	ADO05723	Ado05723
Human ery						
9	828	96.5	1849	12	ADP10351	Adp10351
Reference						
10	828	96.5	1849	13	ACN40465	Acn40465
Tumour-as						
11	828	96.5	1883	2	AAQ05748	Aaq05748 EPO
recep						
12	826.4	96.3	1527	6	ABL51519	Abl51519
Human ery						
13	826.4	96.3	1818	2	AAQ81892	Aaq81892
Human ery						
14	824.8	96.1	1317	3	AAZ49634	Aaz49634
Truncated						
15	823.2	95.9	1585	10	ADE28676	Ade28676
Human NOV						
16	823.2	95.9	1585	12	ADM93421	Adm93421
Human NOV						
17	823.2	95.9	1818	2	AAQ53995	Aaq53995
Human EPO						
18	820	95.6	1317	3	AAZ49636	Aaz49636
Mutant R1						
19	820	95.6	1435	10	ADE28674	Ade28674
Human NOV						
20	820	95.6	1435	12	ADM93419	Adm93419
Human NOV						
21	750.4	87.5	4990	2	AAT48800	Aat48800
Plasmid m						
22	750	87.4	750	2	AAV04434	Aav04434
Erythro						
23	750	87.4	750	2	AAZ30854	Aaz30854
Human ery						
24	748.2	87.2	6256	6	AAL43173	Aal43173
pCAGGS-hS						
25	741	86.4	5565	6	AAL43171	Aal43171
Human exp						
26	700.4	81.6	1666	2	AAX58148	Aax58148
CadC-fusi						
27	577.8	67.3	1740	2	AAQ05747	Aaq05747 EPO
recep						
28	576.4	67.2	5683	6	AAL41116	Aal41116
Plasmid p						

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 05:43:57 ; Search time 2386 Seconds
(without alignments)
13687.822 Million cell

updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgctc.....aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description

1	828	96.5	1759	3	CR592865	CR592865	
full-leng							
2	828	96.5	1797	3	CR620075	CR620075	
full-leng							

3	828	96.5	1811	3	CR618473	CR618473
full-leng						
4	804	93.7	984	5	BX448344	BX448344
BX448344						
5	795.4	92.7	1079	1	AL553257	AL553257
AL553257						
6	788	91.8	1005	5	BX335579	BX335579
BX335579						
7	756	88.1	1527	9	AY414846	AY414846
Homo sapi						
8	737.2	85.9	997	1	AL523468	AL523468
AL523468						
9	714	83.2	1870	3	CR610088	CR610088
full-leng						
10	693.8	80.9	881	1	AL521907	AL521907
AL521907						
11	645.8	75.3	1051	1	AL523895	AL523895
AL523895						
12	630	73.4	902	1	AL523633	AL523633
AL523633						
13	610.4	71.1	816	5	BX406158	BX406158
BX406158						
14	577.6	67.3	1681	3	CR613702	CR613702
full-leng						
15	543.6	63.4	1054	5	BX382171	BX382171
BX382171						
16	501.4	58.4	1452	9	AY414848	AY414848 Mus
muscu						
17	487.8	56.9	853	5	BQ919762	BQ919762
AGENCOURT						
18	446.8	52.1	1009	6	BY710355	BY710355
BY710355						
19	446.8	52.1	1524	3	AK010968	AK010968 Mus
muscu						
20	418.8	48.8	482	5	BQ359730	BQ359730
RC4-HN004						
21	397.8	46.4	1115	9	AY414847	AY414847 Pan
trogl						
22	345.8	40.3	658	6	BY752258	BY752258
BY752258						
23	338.2	39.4	676	2	BE289169	BE289169
601092771						
24	330.8	38.6	592	4	BI344043	BI344043
372394 MA						
25	300.4	35.0	514	4	BI344106	BI344106
372470 MA						
26	288.4	33.6	660	6	BY729758	BY729758
BY729758						
27	285.8	33.3	350	1	AA218796	AA218796
zq97c05.r						
c 28	283	33.0	1082	5	BX382170	BX382170
BX382170						
29	256.2	29.9	383	2	BF661091	BF661091
maa79h04.						
30	252	29.4	840	5	BX360123	BX360123
BX360123						

OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:30:07 ; Search time 507 Seconds
(without alignments)
11315.038 Million cell

updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgtc.....aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	858	100.0	858	19	US-10-625-137-4	Sequence
4, Appli						
2	828	96.5	954	19	US-10-625-137-6	Sequence
6, Appli						
3	828	96.5	987	19	US-10-625-137-8	Sequence
8, Appli						
4	828	96.5	1733	18	US-10-287-971-47	Sequence
47, Appl						
5	828	96.5	1733	18	US-10-287-971-49	Sequence
49, Appl						
6	828	96.5	1818	10	US-09-960-706-693	Sequence
693, App						
7	828	96.5	1818	21	US-10-482-029-191	Sequence
191, App						
8	828	96.5	1849	21	US-10-684-206-23	Sequence
23, Appl						
9	828	96.5	1865	19	US-10-625-137-3	Sequence
3, Appli						
10	826.4	96.3	1527	9	US-09-016-159-4	Sequence 4,
Appli						
11	823.2	95.9	1585	18	US-10-287-971-53	Sequence
53, Appl						
12	820	95.6	1435	18	US-10-287-971-51	Sequence
51, Appl						
13	748.2	87.2	6256	18	US-10-432-305-3	Sequence
3, Appli						
14	741	86.4	804	19	US-10-625-137-10	Sequence
10, Appl						
15	741	86.4	5565	18	US-10-432-305-1	Sequence
1, Appli						
16	739.8	86.2	747	19	US-10-625-137-12	Sequence
12, Appl						
17	576.4	67.2	6122	14	US-10-006-591-1	Sequence
1, Appli						
18	576	67.1	1056	19	US-10-134-188-30	Sequence
30, Appl						
19	576	67.1	1059	19	US-10-134-188-29	Sequence
29, Appl						
20	576	67.1	1121	19	US-10-134-188-26	Sequence
26, Appl						
21	576	67.1	1131	19	US-10-134-188-25	Sequence
25, Appl						
22	576	67.1	4883	14	US-10-006-593-111	Sequence
111, App						

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: September 24, 2005, 06:15:47 ; Search time 141 Seconds
(without alignments)
9956.918 Million cell

updates/sec

Title: US-10-625-137-4
Perfect score: 858
Sequence: 1 atggaccacctcggggcgctc.....aaggctccaggaggaggtga
858

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being
printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	828	96.5	1848	4	US-09-949-016-3882		Sequence
3882, Ap							
2	826.4	96.3	1527	2	US-08-850-293-4		Sequence 4,
Appli							
3	824.8	96.1	1317	3	US-09-339-838-4		Sequence 4,
Appli							
4	820	95.6	1317	3	US-09-339-838-6		Sequence 6,
Appli							

5	750.4	87.5	4990	3	US-08-776-511-1	Sequence 1,
Appli						
6	750	87.4	750	2	US-08-627-151A-9	Sequence 9,
Appli						
7	750	87.4	750	4	US-09-646-691B-7	Sequence 7,
Appli						
8	702	81.8	1666	3	US-09-149-922-4	Sequence 4,
Appli						
9	576	67.1	1056	4	US-10-134-188-30	Sequence
30, Appl						
10	576	67.1	1059	4	US-10-134-188-29	Sequence
29, Appl						
11	576	67.1	1121	4	US-10-134-188-26	Sequence
26, Appl						
12	576	67.1	1131	4	US-10-134-188-25	Sequence
25, Appl						
13	523.4	61.0	774	2	US-08-762-308-9	Sequence 9,
Appli						
14	249	29.0	10546	4	US-09-949-016-15624	Sequence
15624, A						
c 15	52.6	6.1	15447	4	US-09-902-540-1100	Sequence
1100, Ap						
16	49.2	5.7	44377	2	US-08-804-227C-7	Sequence 7,
Appli						
17	49.2	5.7	44377	2	US-08-804-198-1	Sequence 1,
Appli						
18	49	5.7	1794	4	US-09-252-991A-5989	Sequence
5989, Ap						
19	46.8	5.5	999	4	US-09-902-540-8482	Sequence
8482, Ap						
c 20	46.8	5.5	7513	4	US-09-902-540-892	Sequence
892, App						
c 21	46.4	5.4	289	3	US-09-007-005-17	Sequence
17, Appl						
c 22	46.4	5.4	289	3	US-09-244-796-17	Sequence
17, Appl						
23	46.4	5.4	2580	4	US-09-902-540-7003	Sequence
7003, Ap						
c 24	46.4	5.4	4075	4	US-09-902-540-614	Sequence
614, App						
c 25	46.2	5.4	243	4	US-09-252-991A-5899	Sequence
5899, Ap						
26	45.8	5.3	1356	4	US-09-902-540-8249	Sequence
8249, Ap						
27	45.8	5.3	6698	4	US-09-902-540-852	Sequence
852, App						
c 28	45.6	5.3	1053	4	US-09-252-991A-13541	Sequence
13541, A						
29	45.6	5.3	1557	4	US-09-252-991A-13907	Sequence
13907, A						
30	45.6	5.3	1722	4	US-09-252-991A-13800	Sequence
13800, A						
31	45.2	5.3	1926	3	US-09-249-585A-4	Sequence 4,
Appli						
32	45.2	5.3	1931	2	US-09-130-114-2	Sequence 2,
Appli						